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1 ATTTTATTATTACCAATCTTATATAATAATATAATTTCTCTTACAAAAATCTCTAATG 60
61 TTTTATACCTAATATATATATCTGGCTTGATCTACTTTGCACCTCCACTATTTGTTAAT 120
121 TTATTTTCACTATTTTAGGTGTAAT**ATG**AAATTGCAAAAAAATCTTATAACAACACTGCATT 180
M N C K K I L I T T A L
181 AATATCATTAATGTACTCTATTTCCAAGCATATCTTTTCTGTGATACTATACAAGATGGTAA 240
I S L M Y S I P S I S F S D T I Q D G N
241 CATGGGTGGTAACTTCTATATATTAGTGGAAAAGTATGTACCAAGTGTCTCACATTTTGGTAG 300
M G G N F Y I S G K Y V P S V S H F G S
301 CTTCTCAGCTAAAGAAGAAAGCAAAATCAACTGTGGAGTTTGTGGATTAAAAACATGATTG 360
F S A K E E S K S T V G V F G L K H D W
361 GGATGGAAGTCCAATACTTAAAGAATAAACACGCTGACTTTTACTGTTCCAAACATATTCGTT 420
D G S P I L K N K H A D F T V P N Y S F
421 CAGATACGAGAACAAATCCATTCTAGGGTTTGCAGGAGCTATCGGTACTCAATGGGTGG 480
R Y E N N P F L G F A G A I G Y S M G G
481 CCCAAGAATAGAAATTCGAAAATATCTTATGAAGCATTCGACGTAAAAAGTCCTAATATCAA 540
P R I E F E I S Y E A F D V K S P N I N
541 TTATCAAAATGACGCGCACAGGTACTGCGCTCTATCTCATCACACATCGGCAGCCCATGGA 600
Y Q N D A H R Y C A L S H H T S A A M E
601 AGCTGATAAAATTTGTCTTCTTAAAAACGAAGGGTTAATTGACATATCACTTGCAATAAA 660
A D K F V F L K N E G L I D I S L A I N
661 TGCATGTTATGATATAATAAATGACAAAGTACCTGTTTCTCCTTATATATGCGCAGGTAT 720
A C Y D I I N D K V P V S P Y I C A G I

Fig. 1A

721 TGGTACTGATTTGATTTCTATGTTTGAAGCTACAAGTCCATAAAATTTCCCTACCAAGGAAA 780
G T D L I S M F E A T S P K I S Y Q G K
841 CAGGATCATAGGTAATGAGTTTAGAGATATTCCTGCAATAGTACCTAGTAACCTCAACTAC 900
R I I G N E F R D I P A I V P S N S T T
901 AATAAGTGGACCACAAATTTGCAACAGTAACACTAAATGTGTGTCACTTTTGGTTTAGAACT 960
I S G P Q F A T V T L N V C H F G L E L
961 TGGAGGAAGATTTAACTTCTAAATTTTATTGTTGCCACATATTAAAAATGATCTAAACTTG 1020
G G R F N F (SEQ. ID NO: 2)
1021 TTTTAAWTATTGCTACATACAAAAAAGAAAAATAGTGGCAAAAGAAATGTAGCAATAAGA 1080
1081 GGGGGGGGGACCAAAATTTATCTTCTATGCTTCCCAAGTTTTTTCYCGCTATTTATGA 1140
1141 CTTAAACAACAGAAAGTAATATCCTCACGGAAAACTTATCTCAAAATATTTTATTTATTA 1200
1201 CCAATCTTATATAATATAATTAATTTCTCTACAAAAATCACTAGTATTTTATACCAAAA 1260
1261 TATATATTCTGACTTGCTTTTCTTCTGCACTTCTACTATTTTAAATTTATTTGTCACTAT 1320
1321 TAGGTTATAATAAWATGAATTGCMAAAGATTTTTCATAGCAAGTGCATTGATATCACTAA 1380
1381 TGTCTTTCCTTACCCTAGCGTATCTTTTCTGAATCAATACATGAAGATAAATAAATGGTA 1440
1441 ACTTTTACATTAGTGCAAAAGTATATGCCAAGTGCCTCACACTTTGGCGTATTTTCAGTTA 1500
1501 AAGAAAGAGAAAAACAACTGGAGTTTTCGGATTAAACAAGATTGGGACGGAGCAA 1560
1561 CACTAAAGGATGCAAGCAGCAGCCACACAWTAGACCCCAAGTACAATG (SEQ ID NO: 1) 1607

Fig. 1B

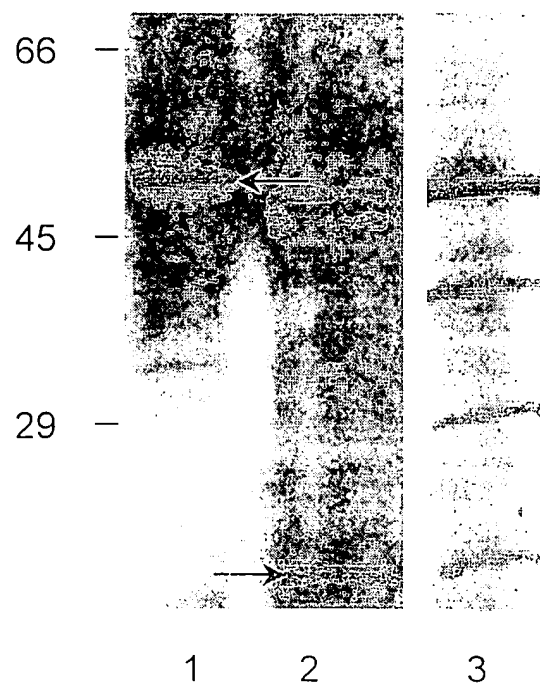


Fig. 2

ECaP28	↓	MNCKKILITLISLMYSIPSISFSDTIQDGNMG-GN----	FYISGKYVPSVSHFGSFAKE-----	ESKSTVGVFGLKH	70
ECa28SA2	VFTIS....SI.FL.NV.Y.NPVYGN.S.-Y.-----	M...P...I...E.-----	K.K.TV.Y...E	70
ECa28SA1		.KY..TFTV...VL.TSFTHF.P.YSPARASTIH--M.TA...I.....	-----QSF.KVLV..DQ	69
EChP28		..Y..VF..S.....IS.L.GV...PA-GSGIN-M.A...V.....	-----RNT.....Q	69
OMP-1B		..Y...FVSS.....SIL.YQ..A.PVTSNDT.INDSREG...	V.N.I...RK...E.APINGNTSI.KK.....K	80
OMP-1C	FF.....ALP.SFL.G.LL.EPV..DSVS-M.A...V.....	-----KNP..ALY...Q	70
OMP-1D		...E.FF.....TL..SFL.G..L..PV..D.IS-M.A...V.....	-----RNT.....IEQ	70
OMP-1E	FF.....V...SFL.G.....PV.GD.IS-V...M.A...M.....	-----KNP..ALY...Q	70
OMP-1F	FF...T.V...SFL.G.....AV.ND.V.-V...Q-----	RNT.T.....Q	70
MAP-1	F...ST....VSFL.GV...V..EE.NPV.S----	V...A..M.TA...KM.I.-----	D.RD.KA.....K	71
VR1					
ECaP28		DWDGSPILKNKHAD-FTVPNYSFRYENNPFLGFAG	IGAIGYSMGGPRIEFIEISYEAFDVKSPNINYQND	AH--RYCALSH--	145
ECa28SA2		N.A.DA.SSQSPD.N..IR...K.AS.K....V.....	I.S...V.M.....NQGN.	(SEQ ID NO: 7)	133
ECa28SA1		RLSHNI.NN.DT.KSLK.Q....K.K.....	I.NS...L.V.H.I..T.N.GN..L..S.--K.....	GS	147
EChP28		N....A.SNSSPN.V...S....K.....	D....L.V...T...NQGN..K.E.-----	---	145
OMP-1B	GDI AQSAN.NRTDPALEFQ..LIS..S.S...A.D....	L.AA.QK..A.N.DN.DT.SGDYK.FG..RED		154
OMP-1C		..N.-VSASSHADAD.NNKG...K.....	V...T...NQGG..K.....	DR--	145
OMP-1D		...RCV.SRTTLS.I.....K....L.S.....	D....L.V...NQGN..K.E.--Y.....	---	146
OMP-1E		..E.-ISSSSHNDNH.NNKG...K.....	V...V...T...NQGN..K.....	GQ--	145
OMP-1F	T.S..SPENT.N....K.....	V..L.N...T...NQGN..K.....	K.Y..T.--	146
MAP-1	VKTPSGNTNSI..EKD...K.....	V...N...V...T...RN.GG..K.....	M.-----	145
VR2					

Fig. 3A

ECaP28	-----HTSAAME-----ADKFFVLKNEGLIDISLAINACYDIINDKVPVSPYICAGIGTDLISMFEATSPKISYQGKLGISY	217
ECa28SA2		133
ECa28SA1	HICSDGNSGDWYTAKT....L....L.V.FML.....TTE.M.F.....T.QN.....LN.	227
EChP28	-----NS.ADMSSASN.....L....FML.....VVGEGI.F.....V.....N.....L...	219
OMP-1B	AI-----ADK.Y.V.....ITFM..MV.T....TAEG..FI..A...V.A...NV.KDFNL.F.....I.....	222
OMP-1C	-----KA.ST---NAT.SHY.L....L....ML.....VVSEGI.F.....V.....IN.....L...	218
OMP-1D	-----LLGTETQIDGAGSAS...I....L.K.FML.....V.SEGI.F.....I.V.....IN.....L...	222
OMP-1E	-----QDNSG---IPKTS.Y.L..S...L....FML.....ESI.L.....V.....N.....L...	218
OMP-1F	-----NSGGKLSNAG.....L....ML.....V.SEGI.F.....V.....IN.....L...	220
MAP-1	-----DT.SSSTAG.TTS.MV...N.T...ML.....ML.GM.....V.....V.VIN..N..L.....	219
	VR3	
ECaP28	SINPETSFIGGHFHRIGNEFRDIPA---IVPSNSTTISGPQF-ATVTNLNVCHFGLGELGGRFNF	278
ECa28SA2		133
ECa28SA1	T..SRV...A....KV....KG..T---LL.DG.NIKVQQS---D.....I.S..F.	287
EChP28	..S..A....KV....T---I.TG..LAGKNYP.I.I.D....I.....A.	281
OMP-1B	P.T..V.A....YY.GV...N.NK..VITPV.LEGAPQTS---L..IDTG..G.V.V..T.	283
OMP-1CA...V....KVA.....ST---LKAFATPSSAATPDL.....S.....V.....	280
OMP-1D	P.S..A....KV....T---MI..E.ALAGKNYP.I...D.FY..I.....QL	286
OMP-1EA....KV....T---LKAFVTSS---ATPDL.I...S.....I.....	278
OMP-1F	..S..A...V....KV.....MI..T..LTGN-H.-TI...S.....V.....	280
MAP-1A.I.....V....K..ATSKVFTS.GNASSAVSPGF.SAI.D.....I.I....V.	284
	VR4	

Fig. 3B

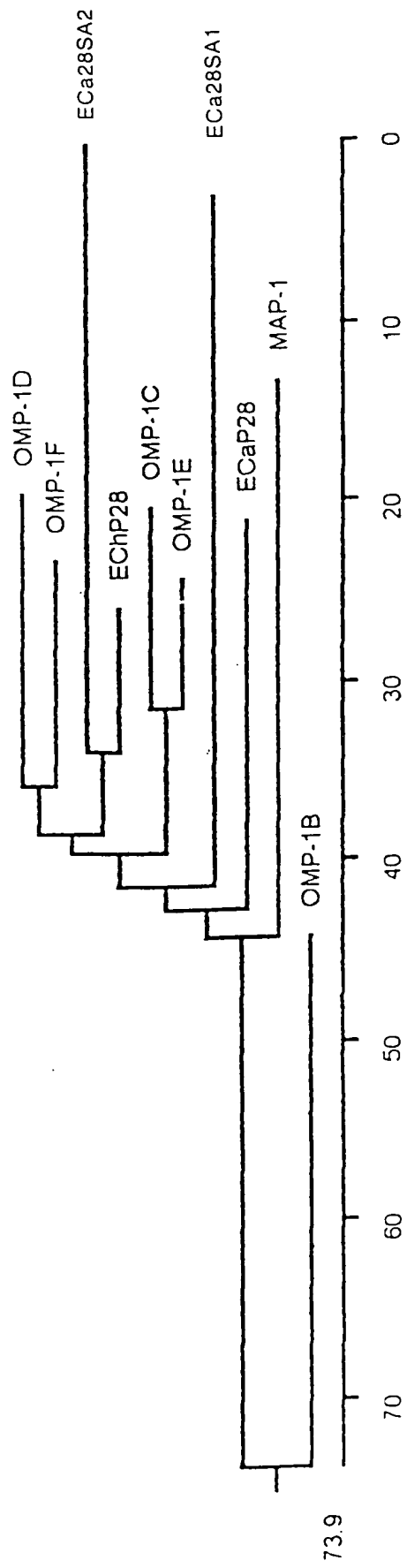


Fig. 4

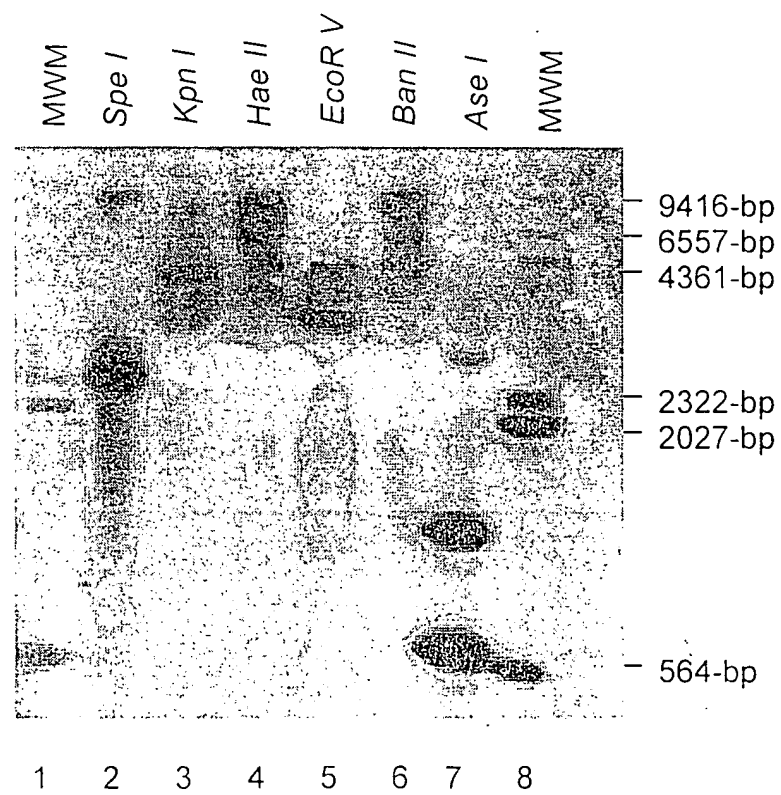
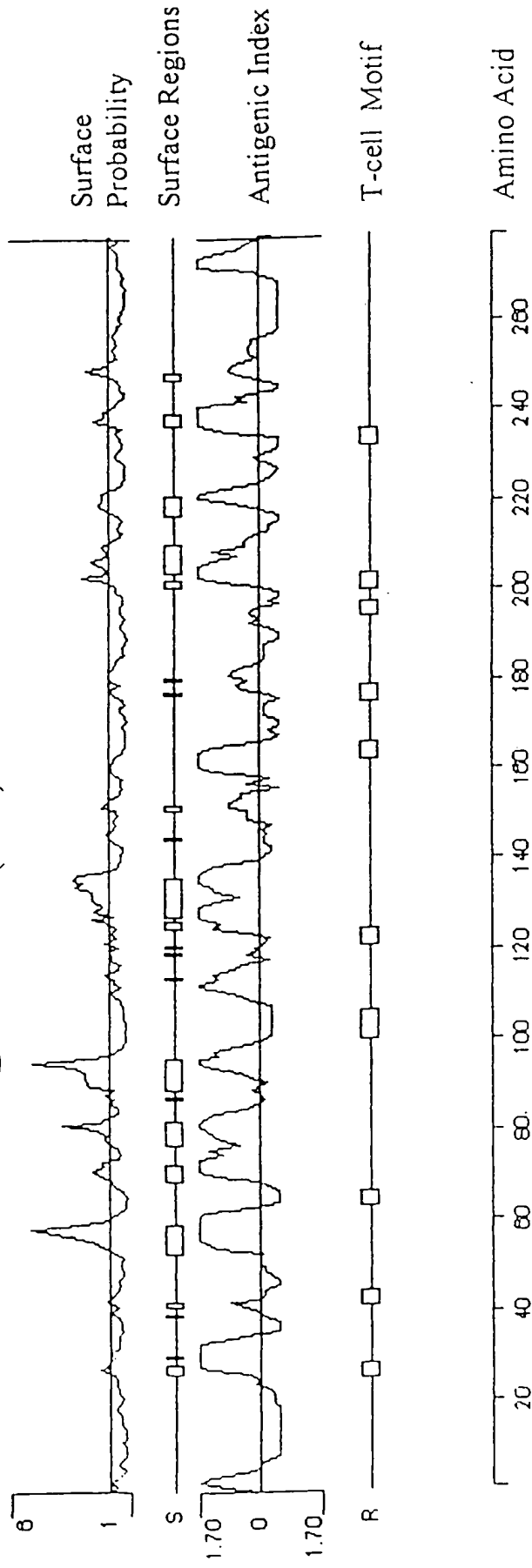


Fig. 5

E. canis P28 (Jake)



E. chaffeensis P28 (Arkansas)

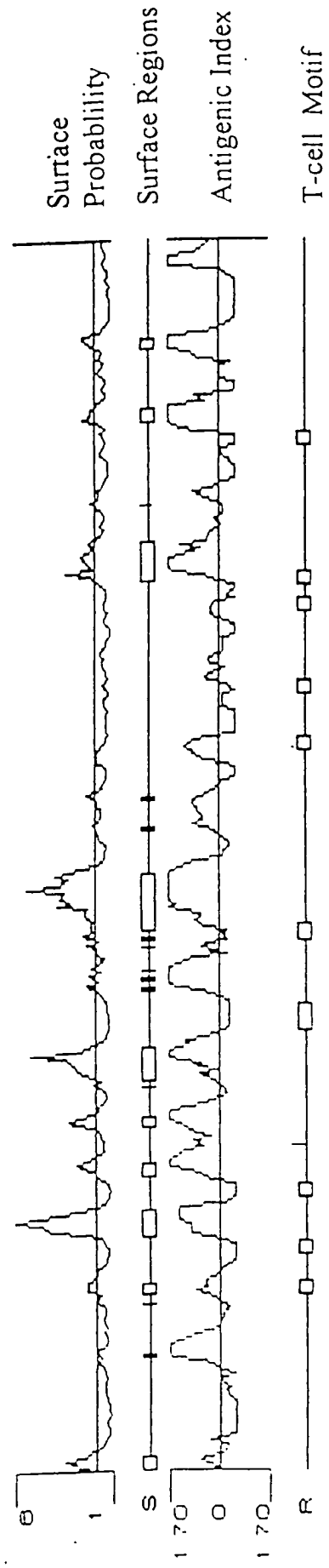


Fig. 6

Eca28SA2

ATGAATTGTAAAAAGTTTTCACAAATAAGTGCATTGATATCATCCATATACTTCCTACCT 60
M N C K K V F T I S A L I S S I Y F L P

AATGTCTCATACTCTAACCCAGTATATGGTAACAGTATGTATGGTAATTTTACATATCA 120
N V S Y S N P V Y G N S M Y G N F Y I S

GGAAGTACATGCCAAGTGTTCCTCATTTTGGAAATTTTTCAGCTGAAGAGAGAAAAAA 180
G K Y M P S V P H F G I F S A E E K K

AAGACAACTGTAGTATATGGCTTAAAGAAAACTGGGCAGGAGATGCCAATACTAGTCAA 240
K T T V V Y G L K E N W A G D A I S S Q

AGTCCAGATGATAATTTTACCATTTCGAAATTTACTCATTTCAAGTATGCAAGCAACAAGTTT 300
S P D D N F T I R N Y S F K Y A S N K F

TTAGGGTTTGCAGTAGCTATTGGTTACTCGATAGGCAGTCCAAAGAAATAGAAGTTGAGATG 360
L G F A V A I G Y S I G S P R I E V E M

TCATTATGAAGCATTTGATGTGAAAAATCCAGGTGATAATTACAAAAACGGTGCTTACAGG 420
S Y E A F D V K N P G D N Y K N G A Y R

TATTGTGCTTTATCTCATCAAGATGATGCGGATGATGACATGACTAGTGCAACTGACAAA 480
Y C A L S H Q D D A D D D M T S A T D K

TTTGTATATTTAATGAAGGATTACTTAACATATCATTTATGACAAAACATATGTTAT 540
F V Y L I N E G L L N I S F M T N I C Y

GAAACAGCAAGCAAAAATATACCTCTCTCTCTTACATATGTGCAGGTATTGGTACTGAT 600
E T A S K N I P L S P Y I C A G I G T D

TTAATTACATGTTGAAACTACACATCCCTAAAAATTTCTTATCAAGGAAAGCTAGGGTTG 660
L I H M F E T T H P K I S Y Q G K L G L

Fig. 7A

GCCTACTTCGTAAGTGCAGAGTCTTCGGTTCTTTGGTATATATTTTCATAAAATTATA 720
 A Y F V S A E S S V S F G I Y F H K I I
 AATAATAAGTTTAAAAATGTTCCAGCCATGGTACCTATTAACTCAGACGAGATAGTAGGA 780
 N N K F K N V P A M V P I N S D E I V G
 CCACAGTTTGCAACAGTAACATTAAATGTATGCTACTTTGGATTAGAACTTGGATGTAGG 840
 P Q F A T V T L N V C Y F G L E L G C R
 TTCAACTTCTAAATTTTCGTGGTACACATATCACGAAGCTAAAATTGTTTTTTTATCTCTGC 900
 F N F * (SEQ ID NO: 4)
 (SEQ ID NO: 3)
 TGTATACAAGAGAAAAATAGTAGTGAATACCTAAACAATATGACAGTACAAGTTTAC 960
 CAAGCTTATTTCTCACAAAACCTTCTTGCTTTTATCTCTTACAAATGAAATGTACACTT 1020
 AGCTTCACTACTGTAGAGTGTGTTTATCAATGCTTTGTTTATTAATACTCTACATAATAT 1080
 GTTAAATTTTCTTACAAAACCTCACTAGTAATTTATATACTAGAAATATATTTCTGACTTGT 1140
 (SEQ ID NO: 31)
Eca28SA3
 ATTTGCTTTTACTTCCACTATTGTTAATTTATTTTCACTATTTTAGGTGTAATATGAAT 1200
 M N
 TGCAAAAAAATTTCTTATAACAACCTGCATTAAATGTCAATTAATGTACTATGCTCCAAGCATA 1260
 C K K I L I T T A L M S L M Y Y A P S I
 TCTTTTCTGATACTATACAAGACGATAACACTGGTAGCTTCTACATCAGTGGAAAAATAT 1320
 S F S D T I Q D D N T G S F Y I S G K Y
 GTACCAAGTGTTCACATTTTGGTGTTTCTCAGCTAAAGAAGAAACTCAACTGTT 1380
 V P S V S H F G V F S A K E E R N S T V
 GGAGTTTGTGGATTAAACATGATTGGAATGGAGGTACAATATCTAACTCTTCTCCAGAA 1440
 G V F G L K H D W N G G T I S N S S P E

Fig. 7B

AATATATTACAGTTCAAAATTATTTCGTTTAAATACGAAAAACAACCCATTCTTAGGGTTT 1500
 N I F T V Q N Y S F K Y E N N P F L G F
 GCAGGAGCTATTGGTTATTCAATGGTGGCCCAAGAAATAGAACTTGAAGTTCTGTACGAG 1560
 A G A I G Y S M G G P R I E L E V L Y E
 ACATTGATGTGAAAAATCAGAAACAATAATTATAAGAACGGCGCACACAGATACTGTGCT 1620
 T F D V K N Q N N N Y K N G A H R Y C A
 TTATCTCATAGTTCAGCAACAAGCATGTCCTCCGCAAGTAACAAATTTGTTTCTTA 1680
 L S H S S A T S M S S A S N K F V F L
 AAAAAATGAAGGTTAATTGACTTATCATTTATGATAAAATGCATGCTATGACATAATAATT 1740
 K N E G L I D L S F M I N A C Y D I I I
 GAAGGAATGCCCTTTTTCACCTTATATTGTGCAGGTGTTGGTACTGATGTTGTTTCCATG 1800
 E G M P F S P Y I C A G V G T D V V S M
 TTTGAAGCTATAAAATCCTAAAATTTCCTTACCAAGGAAAACTAGGATTAGGTTATAGTATA 1860
 F E A I N P K I S Y Q G K L G L G Y S I
 AGTTCAGAAAGCCTCTGTTTATCGGTGGACACTTTCACAGAGTCATAGGTAATGAATTT 1920
 S S E A S V F I G G H F H R V I G N E F
 AGAGACATCCCCGTATGGTTCCCTAGTGGATCAAATCTCCAGAAAAACCAATTTGCAATA 1980
 R D I P A M V P S G S N L P E N Q F A I
 GTAACACTAAATGTGTCACTTTGGCATAGAACTTGGAGGAAGATTAACTTCTGA 2031
 V T L N V C H F G I E L G G R F N F *
 (SEQ ID NO: 5)
 (SEQ ID NO: 6)

Fig. 7C

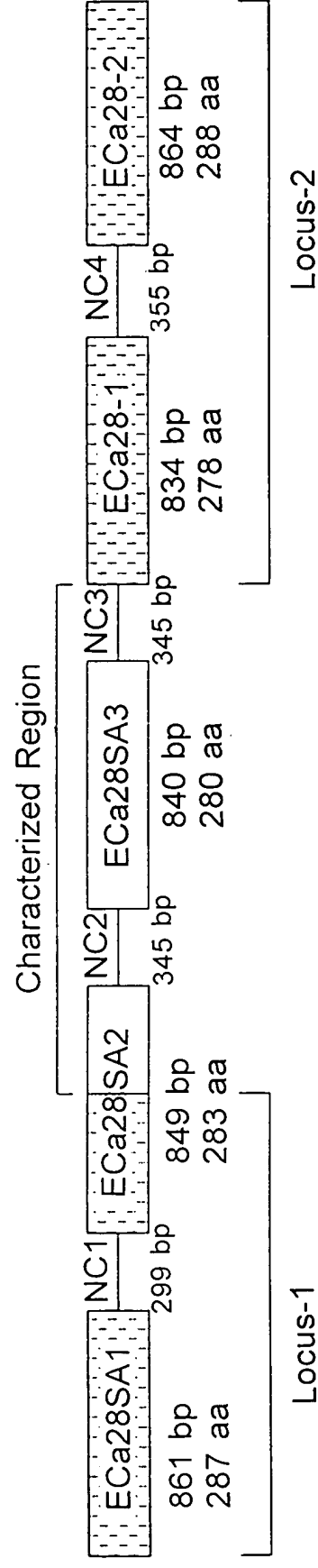


Fig. 8

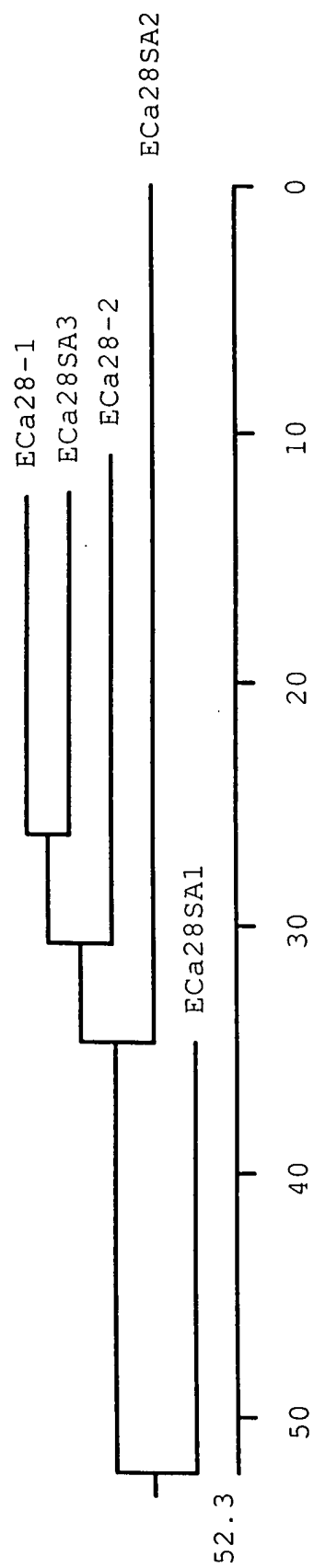


Fig. 9

1	TAATACTTCTATTGT-ACATGTTAAAAATAGTACTAGTTTGTCTTCTGTGGTT--TATAAACGCAAGAGAGAA--	28nc1
1	...TTTCGTGG.A-C...A.C.CG..-GC..AA.T.G.TT.T.A.CTC.GC.G..T..AAG...A.A..TA	28nc2
1	.G..TT.AT.G...CC...A...GA.CTA.AC...T..T.A.TA..GC..C.T..AA..A.A...AA	28nc3
1	...TT.AT.G...CC...A...GA.CTA.AC...T..T.AWTA..GC..C.T..AA..A.A-...AA	28nc4
70	ATAGT-----TAGTAATAAAATTAGAAAG-----TTAAA--TATT---AGAAAAGT-CA	28nc1
72	G...G--AAATTACC.AC...TGAC..T.CAAGTTTACC..GCT...CTC.C...C.T.T	28nc2
75	...GGCAAAAGAATG...C...GAGG.GGG.GGGGAC...TT..CCTTC--T.TTC.T.T	28nc3
74	...GGCAAAAGAATG...C...GAGG.GGG.GGGGACC...TT...CTTC--T.TGC.T.C	28nc4
112	TATGTTTTTTCATTGTCAATTGAT-ACTCAACTA-----AAAGTAGTAT-----AAATGT-----	28nc1
136	.G...C...T..CTCT--T.CA.-G..A.-GTAC.-CT...CT.CACTACTGTAG.G...GTTTATCAATGC	28nc2
139	A..A..C..T--ACT...-----T...A..GCAC..CTC.A.GCTTCCA-GG-A...A.GT-TTCTAATAT	28nc3
138	C.A...TCYC.CT...T..G...T..AC.ACAG..G...A...CCTCACGG-A...CT.ATCTTCAAAATAT	28nc4
159	--TACTTATTAATAAT-TTTACGTTAGTATATTAATAATTTCCCTTACAAAAAGCCACTAGTATTTTATA	28nc1
205	TT.GT.....-C.C..A..A..G.....TT.....CT.....A.....	28nc2
202	TT..T.....CC..CC..TA..A.....T.....AT.T...A.G.....	28nc3
211	TT..T.....CC..C-..TA..A.....T.....AT.....	28nc4
222	CTAAAAGC-TATACTTTGGCTTGTATTTAAATTTGTATTTTACTACTGTAAATTTACTT-TCACTGTT--TCT	28nc1
269	..T.G.ATA...T.C..A.....GC...A..C.CC...T.....T...A...A...A...TA	28nc2
268	..T..TATA...T.C.....C...C.C.CC...T.....T...A...A...A...TA	28nc3
276	.C-...ATA...T.C..A...CT...CT.C.C.C.C.C...T.T.....T.G...A..AGG.TA	28nc4
-35		
292	GGTGTAAT 28nc1 (SEQ ID NO: 30)	
338- 28nc2 (SEQ ID NO: 31)	
339- 28nc3 (SEQ ID NO: 32)	
339	TA-A...-W 28nc4 (SEQ ID NO: 33)	
RBS		
-10		

Fig. 10

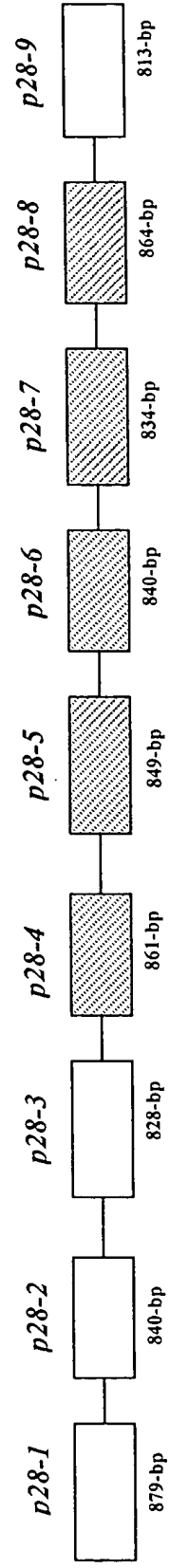


Fig. 11

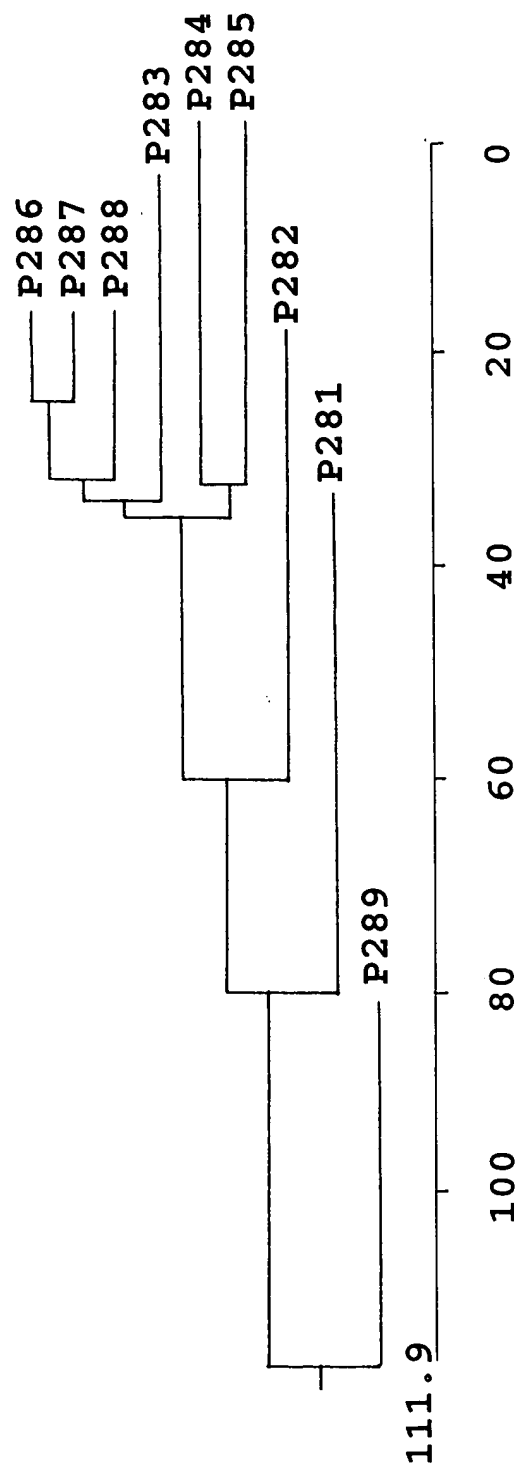


Fig. 12

ATGAATAATAAACTCAAATTTACTATAATAAACACAGTATTAGTATGCTTATTGTCATTA 60
 M N N K L K F T I I N T V L V C L L S L

CCTAATATATCTTCCTCAAAGGCCATAAACAAATAACGCTAAAAAGTACTACGGATTATAT 120
 P N I S S S K A I N N N A K K Y Y G L Y

ATCAGTGGACAATATAAACCCAGTGTTTCTGTTTTTCAGTAATTTTTTCAGTTAAAGAAACC 180
 I S G Q Y K P S V S V F S N F S V K E T

AATGTCATAACTAAAAACCTTATAGCTTTAAAAAAGATGTTGACTCTATTGAAACCAAG 240
 N V I T K N L I A L K K D V D S I E T K

ACTGATGCCAGTGTAGGTATTAGTAACCCATCAAATTTTACTATCCCCTATACAGCTGTA 300
 T D A S V G I S N P S N F T I P Y T A V

TTTCAAGATAATTCTGTCAATTTCAATGGAAGTATTGGTTACACCTTTGCTGAAGGTACA 360
 F Q D N S V N F N G T I G Y T F A E G T

AGAGTTGAAATAGAAGGTTCTTATGAGGAATTTGATGTTAAAAACCCTGGAGGCTATACA 420
 R V E I E G S Y E E F D V K N P G G Y T

CTAAGTGATGCCTATCGCTATTTTGCATTAGCACGTGAAATGAAAGGTAATAGTTTTTACA 480
 L S D A Y R Y F A L A R E M K G N S F T

CCTAAAGAAAAAGTTTCTAATAGTATTTTTCACACTGTAATGAGAAATGATGGATTATCT 540
 P K E K V S N S I F H T V M R N D G L S

ATAATATCTGTTATAGTAAATGTTTGCTACGATTTCTCTTTGAACAATTTGTCAATATCG 600
 I I S V I V N V C Y D F S L N N L S I S

CCTTACATATGTGGAGGAGCAGGGGTAGATGCTATAGAATTCTTCGATGTATTACACATT 660
 P Y I C G G A G V D A I E F F D V L H I

AAGTTTGCATATCAAAGCAAGCTAGGTATTGCTTATTCTCTACCATCTAACATTAGTCTC 720
 K F A Y Q S K L G I A Y S L P S N I S L

TTTGCTAGTTTATATTACCATAAAGTAATGGGCAATCAATTTAAAAATTTAAATGTCCAA 780
 F A S L Y Y H K V M G N Q F K N L N V Q

CATGTTGCTGAACTTGCAAGTATACCTAAAATTACATCCGCAGTTGCTACACTTAATATT 840
 H V A E L A S I P K I T S A V A T L N I

GGTTATTTTGGAGGTGAAATTGGTGCAAGATTGACATTT (SEQ ID No. 39) 879
 G Y F G G E I G A R L T F (SEQ ID NO. 40)

Fig. 13

ATGAATTATAAGAAAATTCTAGTAAGAAGCGCGTTAATCTCATTAAATGTCAATCTTACCA 60
 M N Y K K I L V R S A L I S L M S I L P
 TATCAGTCTTTTGCAGATCCTGTAGGTTCAAGAACTAATGATAACAAAGAAGGCTTCTAC 120
 Y Q S F A D P V G S R T N D N K E G F Y
 ATTAGTGCAAAGTACAATCCAAGTATATCACACTTTAGAAAATTCTCTGCTGAAGAACT 180
 I S A K Y N P S I S H F R K F S A E E T
 CCTATTAATGGAACAAATTCTCTCACTAAAAAGTTTTCGGACTAAAGAAAGATGGTGAT 240
 P I N G T N S L T K K V F G L K K D G D
 ATAACAAAAAAGACGATTTTACAAGAGTAGCTCCAGGCATTGATTTTCAAATAACTTA 300
 I T K K D D F T R V A P G I D F Q N N L
 ATATCAGGATTTTTCAGGAAGTATTGGTTACTCTATGGACGGACCAAGAATAGAACTTGAA 360
 I S G F S G S I G Y S M D G P R I E L E
 GCTGCATATCAACAATTTAATCCAAAAACACCGATAACAATGATACTGATAATGGTGAA 420
 A A Y Q Q F N P K N T D N N D T D N G E
 TACTATAAACATTTTGCATTATCTCGTAAAGATGCAATGGAAGATCAGCAATATGTAGTA 480
 Y Y K H F A L S R K D A M E D Q Q Y V V
 CTTAAAAATGACGGCATAACTTTTATGTCATTGATGGTTAATACTTGCTATGACATTACA 540
 L K N D G I T F M S L M V N T C Y D I T
 GCTGAAGGAGTATCTTTTCGTACCATATGCATGTGCAGGTATAGGAGCAGATCTTATCACT 600
 A E G V S F V P Y A C A G I G A D L I T
 ATTTTTAAAGACCTCAATCTAAAATTTGCTTACCAAGGAAAAATAGGTATTAGTTACCCT 660
 I F K D L N L K F A Y Q G K I G I S Y P
 ATCACACCAGAAGTCTCTGCATTTATTGGTGGATACTACCATGGCGTTATTGGTAATAAA 720
 I T P E V S A F I G G Y Y H G V I G N K
 TTTGAGAAGATACCTGTAATAACTCCTGTAGTATTAAATGATGCTCCTCAAACCACATCT 780
 F E K I P V I T P V V L N D A P Q T T S
 GCTTCAGTAACTCTTGACGTTGGATACTTTGGCGGAGAAATTGGAATGAGGTTACCTTC 840
 A S V T L D V G Y F G G E I G M R F T F
 (SEQ ID No. 41)
 (SEQ ID No. 42)

Fig. 14

ATGAACTGTAAAAAATTCTTATAACAACACTACATTGGTATCACTAACAATTCTTTTACCT 60
 M N C K K I L I T T T L V S L T I L L P
 GGCATATCTTTCTCCAAACCAATACATGAAAACAATACTACAGGAACTTTTACATTATT 120
 G I S F S K P I H E N N T T G N F Y I I
 GGAAAATATGTACCAAGTATTTTCACATTTTGGGAACTTTTCAGCTAAAGAAGAAAAAAC 180
 G K Y V P S I S H F G N F S A K E E K N
 ACAACAACCTGGAATTTTTGGATTAAAAGAATCATGGACTGGTGGTATCATCCTTGATAAA 240
 T T T G I F G L K E S W T G G I I L D K
 GAACATGCAGCTTTTAATATCCCAAATTATTCATTTAAATATGAAAATAATCCATTTTTA 300
 E H A A F N I P N Y S F K Y E N N P F L
 GGATTTGCAGGGGTAATTGGCTATTCAATAGGTAGTCCAAGAATAGAATTTGAAGTATCA 360
 G F A G V I G Y S I G S P R I E F E V S
 TACGAGACATTCGATGTACAAAATCCAGGAGATAAGTTTAAACAATGATGCACATAAGTAT 420
 Y E T F D V Q N P G D K F N N D A H K Y
 TGTGCTTTATCCAATGATTCCAGTAAAACAATGAAAAGTGGTAAATTCGTTTTTCTCAA 480
 C A L S N D S S K T M K S G K F V F L K
 AATGAAGGATTAAGTGACATATCACTCATGTAAATGTATGTTATGATATAATAAACAAA 540
 N E G L S D I S L M L N V C Y D I I N K
 AGAATGCCTTTTTTCACCTTACATATGTGCAGGCATTGGTACTGACTTAATATTCATGTTT 600
 R M P F S P Y I C A G I G T D L I F M F
 GACGCTATAAACCATAAAGCTGCTTATCAAGGAAAATTAGGTTTTAATTATCCAATAAGC 660
 D A I N H K A A Y Q G K L G F N Y P I S
 CCAGAAGCTAACATTTCTATGGGTGTGCACTTTCACAAAGTAACAAACAACGAGTTTAGA 720
 P E A N I S M G V H F H K V T N N E F R
 GTTCCTGTTCTATTAAGTCTGGAGGACTCGCTCCAGATAATCTATTTGCAATAGTAAAG 780
 V P V L L T A G G L A P D N L F A I V K
 TTGAGTATATGTCATTTTGGGTTAGAATTTGGGTACAGGGTCAGTTTT (SEQ ID No. 43) 828
 L S I C H F G L E F G Y R V S F (SEQ ID NO. 44)

Fig. 15

ATGAATTACAAAAGATTTGTTGTAGGTGTTACGCTGAGTACATTTGTTTTTTTCTTATCT 60
 M N Y K R F V V G V T L S T F V F F L S

GATGGTGCTTTTTCTGATGCAAATTTTTCTGAAGGGAGGAGAGGACTTTATATAGGTAGT 120
 D G A F S D A N F S E G R R G L Y I G S

CAGTATAAAGTTGGTATTCCCAATTTTAGTAATTTTTTCAGCTGAAGAAACAATTCCTGGT 180
 Q Y K V G I P N F S N F S A E E T I P G

ATTACAAAAAAGATTTTTGCGTTAGGTCTTGATAAGTCTGAGATAAATACTCACAGCAAT 240
 I T K K I F A L G L D K S E I N T H S N

TTTACACGATCATATGACCCTACTTATGCAAGCAGTTTTGCAGGGTTTAGTGGTATCATT 300
 F T R S Y D P T Y A S S F A G F S G I I

GGATATTATGTTAATGACTTTAGGGTAGAATTTGAAGGTTCTTATGAGAATTTTGAACCT 360
 G Y Y V N D F R V E F E G S Y E N F E P

GAAAGACAATGGTACCCTGAGAATAGCCAAAGCTACAAATTTTTTGCTTTGTCTCGAAAT 420
 E R Q W Y P E N S Q S Y K F F A L S R N

GCTACAAATAGTGATAATAAGTTTATAGTACTAGAGAATAACGGCGTTGTTGACAAGTCT 480
 A T N S D N K F I V L E N N G V V D K S

CTTAATGTAAATGTTTGTATGATATTGCTAGTGGTAGTATTCCTTTAGCACCTTATATG 540
 L N V N V C Y D I A S G S I P L A P Y M

TGTGCTGGTGTGGTGCAGATTATATAAAGTTTTTAGGTATATCATTGCCTAAGTTTTCT 600[^]
 C A G V G A D Y I K F L G I S L P K F S

TATCAAGTTAAGTTTGGTGTCAACTACCCTCTAAATGTTAATACTATGTTGTTTGGTGGG 660
 Y Q V K F G V N Y P L N V N T M L F G G

GGTTATTACCATAAGGTTGTAGGTGATAGGCATGAGAGAGTAGAAATAGCTTACCATCCT 720
 G Y Y H K V V G D R H E R V E I A Y H P

ACTGCATTATCTGACGTTCCTAGAACTACTTCAGCTTCTGCTACTTTAAATACTGATTAT 780
 T A L S D V P R T T S A S A T L N T D Y

TTTGGTTGGGAGATTGGATTTAGATTTGCGCTA (SEQ ID No. 45) 813
 F G W E I G F R F A L (SEQ ID No. 46)

Fig. 16